What is claimed:

1. A method of detecting whether a subject is either predisposed to or afflicted with a pulmonary disease which comprises (1) obtaining a suitable sample from the subject; and (2) detecting in the sample a bone morphogenetic protein receptor-II mutation which is not present in wildtype bone morphogenetic protein receptor-II,

wherein the presence of a mutation indicates that the subject is predisposed to or afflicted with the pulmonary disease.

2. The method of claim 1, wherein the suitable sample is a nucleic acid sample, and the mutation is detected in a nucleic acid encoding bone morphogenetic protein receptor-II.

3. The method of claim 1, wherein the suitable sample is one which comprises a bone morphogenetic protein receptor-II polypeptide, and the mutation is detected in the bone morphogenetic protein receptor-II polypeptide.

4. The method of claim 1, wherein the pulmonary disease is Primary Pulmonary Hypertension.

5. The method of claim 4, wherein the Primary Pulmonary Hypertension is Familial Primary Pulmonary

Hypertension.

6. The method of claim 1, wherein a bone morphogenetic protein receptor-II polypepetide is encoded by a gene which is located on chromosome 2q34.

7. The method of claim 1, wherein a wildtype nucleic acid encoding a bone morphogenetic protein receptor-II polypepetide comprises consecutive nucleotides comprising the nucleic acid sequence set forth in SEQ ID NO: 1.

8. The method of claim 1, wherein a wildtype bone morphogenetic protein receptor-II polypeptide comprises consecutive amino acids comprising the amino acid sequence set forth in SEQ ID NO: 2.

9. The method of claim 1, wherein the mutation results in a truncated bone morphogenetic protein receptor-II.

10. The method of claim 2, wherein the mutated nucleic acid comprises a deletion of a nucleotide segment guanosine-guanosine-guanosine-guanosine-adenosine located at positions 1099-1103 in a wildtype nucleic acid, which wildtype nucleic acid comprises the sequence set forth in SEQ ID NO:1.

11. The method of claim 3, wherein the mutated bone

morphogenetic protein receptor-II polypeptide comprises a frameshift mutation at a glutamic acid residue located at position 368 in the wildtype polypeptide, which wildtype polypeptide comprises the amino acid sequence set forth in SEQ ID NO:2.

12. The method of claim 2, wherein the mutated nucleic acid comprises a deletion of a thymidine residue located at position 2579 in a wildtype nucleic acid, which wildtype nucleic acid comprises the sequence set forth in Seq ID NO:1.

13. The method of claim 3, wherein the mutated bone morphogenetic protein receptor-II polypeptide comprises a frameshift mutation at an asparagine residue located at position 861 in the wildtype polypeptide, which wildtype polypeptide comprises the amino acid sequence set forth in SEQ ID NO:2.

14. The method of claim 2, wherein the mutated nucleic acid comprises a replacement of a nucleotide segment cytosine-thymidine-thymidine-thymidine located at positions 507-510 in a wildtype nucleic acid with a nucleotide segment adenosine-adenosine-adenosine, which wildtype nucleic acid comprises the sequence set forth in SEQ ID NO:1.

15. The method of claim 3, wherein the mutated bone morphogenetic protein receptor-II polypeptide comprises a mutation of a cysteine located at position 169 in a wildtype polypeptide to a termination codon, which

wildtype polypeptide comprises the sequence set forth in SEQ ID NO:2.

16. The method of claim 2, wherein the mutated nucleic acid comprises a mutation of a cytosine located at position number 2617 in a wildtype nucleic acid to a thymidine, which wildtype nucleic acid comprises the sequence set forth in SEQ ID NO:1.

17. The method of claim 3, wherein the mutated bone morphogenetic protein receptor-II polypeptide comprises a mutation of an arginine located at position 873 in a wiltype polypeptide to a termination codon, which wildtype polypeptide comprises the sequence set forth in SEQ ID NO:2.

18. The method of claim 2, wherein the mutated nucleic acid comprises a replacement of a nucleotide segment adenosine-guanosine present at positions 690-691 in a wildtype nucleic acid with a thymidine residue, which wildtype nucleic acid comprises the sequence set forth in SEQ ID NO:1.

19. The method of claim 3, wherein the mutated bone morphogenetic protein receptor-II polypeptide comprises a frameshift mutation at a lysine residue located at position 230 in a wildtype polypeptide, which wildtype polypeptide comprises the sequence set forth in SEQ ID NO:2.

20. The method of claim 2, wherein the mutation is a missense mutation.

21. The method of claim 2, wherein the mutated nucleic acid comprises a mutation of a cytosine located at position number 1471 in a wildtype nucleic acid to a thymidine, which wildtype nucleic acid comprises the sequence set forth in SEQ ID NO:1.

22. The method of claim 3, wherein the mutated bone morphogenetic protein receptor-II polypeptide comprises a mutation of an arginine located at position 491 in a wildtype polypeptide to a tryptophan, which wildtype polypeptide has the sequence set forth in SEQ ID NO:2.

23. The method of claim 2, wherein the mutated nucleic acid comprises a mutation of a guanosine located at position number 1472 in a wildtype nucleic acid to an adenosine, which wildtype nucleic acid comprises the sequence set forth in SEQ ID NO:1.

24. The method of claim 3, wherein the mutated bone morphogenetic protein receptor-II polypepetide comprises a mutation of an arginine located at position number 491 in a wildtype polypeptide to a glutamine, which wildtype polypeptide has the sequence set forth in SEQ ID NO:2.

25. The method of claim 2, wherein the mutated nucleic acid comprises a deletion of a nucleotide segment adenosine-thymidine-thymidine-thymidine located at positions 1248-1251 in a wildtype nucleic acid, which wildtype nucleic acid comprises the sequence set forth in SEQ ID NO:1.

26. The method of claim 3, wherein the mutated bone morphogenetic protein receptor-II polypepetide comprises a mutation of an phenylalanine located at position number 417 in a wildtype polypeptide to a stop codon, which wildtype polypeptide has the sequence set forth in SEQ ID NO:2.

27. The method of claim 2, wherein the mutated nucleic acid comprises a mutation of a cytosine located at position number 994 in a wildtype nucleic acid to a thymidine, which wildtype nucleic acid comprises the sequence set forth in SEQ ID NO:1.

28. The method of claim 3, wherein the mutated bone morphogenetic protein receptor-II polypepetide comprises a mutation of an arginine located at position number 332 in a wildtype polypeptide to a stop codon, which wildtype polypeptide has the sequence set forth in SEQ ID NO:2.

29. The method of claim 2, wherein the mutated nucleic acid comprises a mutation of a thymidine located at position number 295 in a wildtype nucleic acid to a cytosine, which wildtype nucleic acid comprises the sequence set forth in SEQ ID NO:1.

30. The method of claim 3, wherein the mutated bone morphogenetic protein receptor-II polypepetide comprises a mutation of a cysteine located at position number 99 in a wildtype polypeptide to an arginine, which wildtype polypeptide has the sequence set forth in SEQ ID NO:2.

31. The method of claim 2, wherein the mutated nucleic acid comprises a deletion of a guanosine residue located at position 1097 in a wildtype nucleic acid, which wildtype nucleic acid comprises the sequence set forth in Seq ID NO:1.

32. The method of claim 3, wherein the mutated bone morphogenetic protein receptor-II polypeptide comprises a frameshift mutation at a proline residue located at position 366 in the wildtype polypeptide, which wildtype polypeptide comprises the amino acid sequence set forth in SEQ ID NO:2.

33. The method of claim 2, wherein the mutated nucleic acid comprises a mutation of a guanosine located at position number 727 in a wildtype nucleic acid to a thymidine,

which wildtype nucleic acid comprises the sequence set forth in SEQ ID NO:1.

34. The method of claim 3, wherein the mutated bone morphogenetic protein receptor-II polypepetide comprises a mutation of a glutamic acid located at position number 243 in a wildtype polypeptide to a stop codon, which wildtype polypeptide has the sequence set forth in SEQ ID NO:2.

35. The method of claim 2, wherein the mutated nucleic acid comprises a deletion of an adenosine residue located at position 1214 in a wildtype nucleic acid, which wildtype nucleic acid comprises the sequence set forth in Seq ID NO:1.

36. The method of claim 3, wherein the mutated bone morphogenetic protein receptor-II polypeptide comprises a frameshift mutation at an aspartic acid residue located at position 405 in the wildtype polypeptide, which wildtype polypeptide comprises the amino acid sequence set forth in SEQ ID NO:2.

37. The method of claim 2, wherein the mutated nucleic acid comprises a deletion of a nucleotide segment adenosine-cytosine located at positions 2441-2442 in a wildtype nucleic acid, which wildtype nucleic acid comprises the sequence set forth in SEQ ID NO:1.

38. The method of claim 3, wherein the mutated bone morphogenetic protein receptor-II polypeptide comprises

a frameshift mutation at a histidine residue located at position 814 in the wildtype polypeptide, which wildtype polypeptide comprises the amino acid sequence set forth in SEQ ID NO:2.

39. The method of claim 2, wherein the mutated nucleic acid comprises a mutation of a cytosine located at position number 2695 in a wildtype nucleic acid to a thymidine, which wildtype nucleic acid comprises the sequence set forth in SEQ ID NO:1.

40. The method of claim 3, wherein the mutated bone morphogenetic protein receptor-II polypepetide comprises a mutation of an arginine located at position number 899 in a wildtype polypeptide to a stop codon, which wildtype polypeptide has the sequence set forth in SEQ ID NO:2.

41. The method of claim 2, wherein the mutated nucleic acid comprises a deletion of a nucleotide segment present at positions 189-209 in a wildtype nucleic acid, which wildtype nucleic acid comprises the sequence set forth in SEQ ID NO:1.

42. The method of claim 3, wherein the mutated bone morphogenetic protein receptor-II polypepetide comprises a deletion of an amino acid segment serine-threonine-cysteine-tyrosine-glycine-leucine-tryptophan located at position numbers 64-70 in a wildtype polypeptide, which wildtype polypeptide has the sequence set forth in SEQ ID NO:2.

43. The method of claim 2, wherein the mutated nucleic acid comprises a mutation of a guanosine located at position number 296 in a wildtype nucleic acid to a adenosine, which wildtype nucleic acid comprises the sequence set forth in SEQ ID NO:1.

44. The method of claim 3, wherein the mutated bone morphogenetic protein receptor-II polypepetide comprises a mutation of a cysteine located at position number 99 in a wildtype polypeptide to a tyrosine, which wildtype polypeptide has the sequence set forth in SEQ ID NO:2.

45. The method of claim 2, wherein the mutated nucleic acid comprises a mutation of a thymidine located at position number 250 in a wildtype nucleic acid to a cytosine, which wildtype nucleic acid comprises the sequence set forth in SEQ ID NO:1.

46. The method of claim 3, wherein the mutated bone morphogenetic protein receptor-II polypepetide comprises a mutation of a cysteine located at position number 84 in a wildtype polypeptide to an arginine, which wildtype polypeptide has the sequence set forth in SEQ ID NO:2.

47. The method of claim 2, wherein the mutated nucleic acid comprises a mutation of a guanosine located at position number 1040 in a wildtype nucleic acid to a adenosine, which wildtype nucleic acid comprises the sequence set forth in SEQ ID NO:1.

48. The method of claim 3, wherein the mutated bone

morphogenetic protein receptor-II polypepetide comprises a mutation of a cysteine located at position number 347 in a wildtype polypeptide to a tyrosine, which wildtype polypeptide has the sequence set forth in SEQ ID NO:2.

49. The method of claim 5, wherein the subject is suffering from an asthmatic symptom, so as to thereby prevent a subject afflicted with Familial Primary Pulmonary Hypertension from being misdiagnosed as asthmatic.

50. The method of claim 49, wherein the asthmatic symptom is wheezing or intermittent shortness of breath.

51. A method of predicting an increased likelihood of a subject giving birth to twins or triplets which comprises:

a) obtaining a suitable nucleic acid sample from the subject;

b) detecting the presence of one copy of a mutant nucleic acid which encodes a bone morphogenetic protein receptor-II polypeptide, thereby indicating that the subject is heterozygous for the mutation,

wherein heterozygosity predicts an increased likelihood of the subject giving birth to twins or triplets.

52. A method of predicting an increased likelihood of a

subject having a miscarriage prior to giving birth to a child which comprises:

a) obtaining a suitable nucleic acid sample from the subject;

b) detecting the presence of two copies of a mutant nucleic acid which encodes a bone morphogenetic protein receptor-II polypeptide, thereby indicating that the subject is homozygous for the mutation,

wherein homozygosity predicts an increased likelihood of the subject having a miscarriage prior to giving birth to a child.

53. A method of preventing and/or treating Familial Primary Pulmonary Hypertension in a subject which comprises introducing a nucleic acid encoding a wildtype bone morphogenetic protein receptor-II polypeptide operably linked to a promotor into a suitable cell under conditions such that the nucleic acid expresses the wildtype bone morphogenetic protein receptor-II protein so as to thereby prevent and/or treat Familial Primary Pulmonary Hypertension in the subject.

54. The method of claim 53, wherein the suitable cell is a lung cell.

55. A method of preventing and/or treating Familial Primary Pulmonary Hypertension in a subject which comprises administering to the subject an effective amount of a

wildtype bone morphogenetic protein receptor-II polypeptide comprising consecutive amino acids having the sequence set forth in SEQ ID NO:2 to prevent and/or treat Familial Primary Pulmonary Hypertension in the subject.

56. A method of detecting whether a subject is either predisposed to or afflicted with Familial Primary Pulmonary Hypertension which comprises:

a) obtaining a suitable nucleic acid sample from the subject; and

b) detecting the presence of a $(GGC)_{12}$ trinucleotide repeat at positions -928 to -963 in the 5' end of the bone morphogenetic protein receptor-II gene,

wherein the presence of the trinucleotide repeat indicates that the subject is either predisposed to or afflicted with Familial Primary Pulmonary Hypertension.

57. A method of screening for a compound capable of treating Familial Primary Pulmonary Hypertension which comprises:

a) contacting a cell which expresses a mutant bone morphogenetic protein receptor-II with the compound; and

b) determining whether the compound is capable of reversing the functional deficit present in Familial Primary Pulmonary Hypertension in the cell,

wherein a reversal of the functional deficit in the

cell indicates that the compound is capable of treating Familial Primary Pulmonary Hypertension.

58. The method of claim 57, wherein the functional deficit is reduced kinase activity for the bone morphogenetic protein receptor-II.

59. A method of obtaining a composition which comprises:

a) identifying a compound capable of treating Familial Primary Pulmonary Hypertension by the method of claim 57; and

b) admixing the compound so identified or a homolog or derivative thereof with a carrier.

60. A transgenic non-human animal whose cells comprise a mutant nucleic acid which encodes a bone morphogenetic protein receptor-II polypeptide.

61. The transgenic non-human animal of claim 60, wherein the non-human animal exhibits primary pulmonary hypertension.

62. The transgenic non-human animal of claim 60, wherein the nucleic acid is operatively linked to a promotor.

63. The transgenic non-human animal of claim 60, wherein the non-human animal is a mouse, a rat, a sheep, a dog, a primate or a reptile.